Figure 1: Restriction pattern of the HAL coding region cut with selected enzymes.

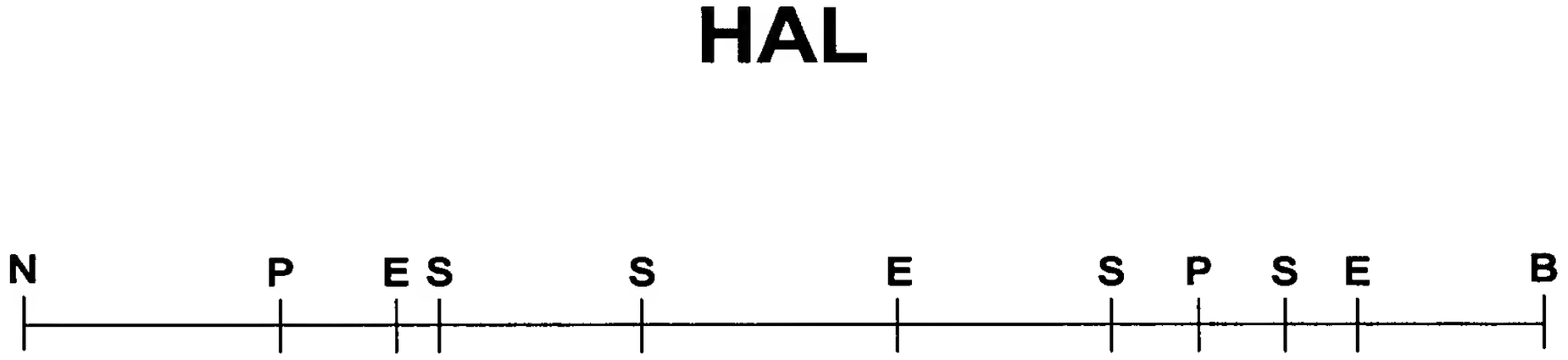

Figure 2: Experimentally derived peptide sequences of HAL

N-terminal

(M)ASAPQITLGLSGATAD

Internal

(M)ALADLDELLDEA

(M)GEPVEREVLRA

Figure 3: SphI digestion pattern of HAL gene showing oligonucleotide and subclones.

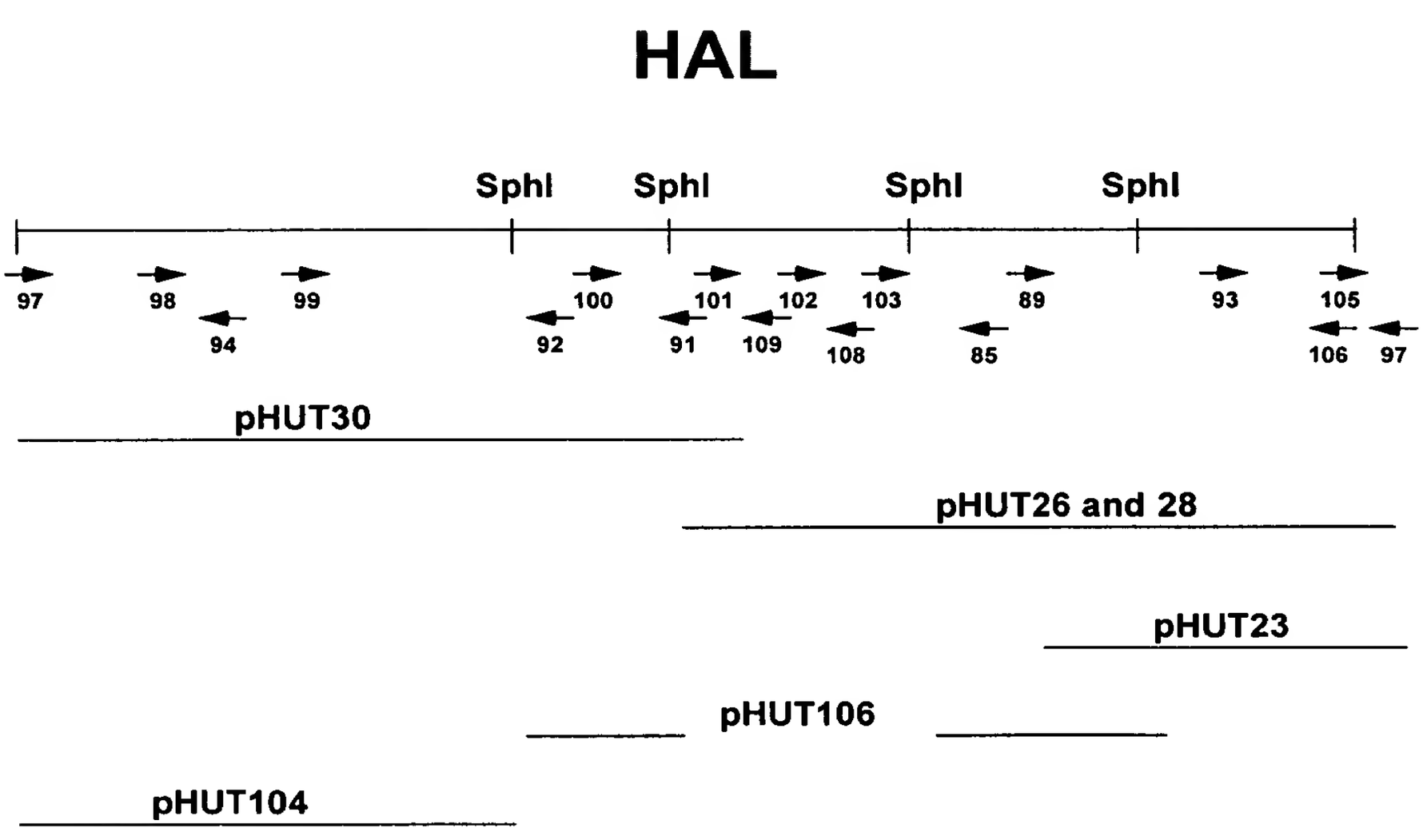

Figure 4: Histidine ammonia lyase overexpressing plasmid.

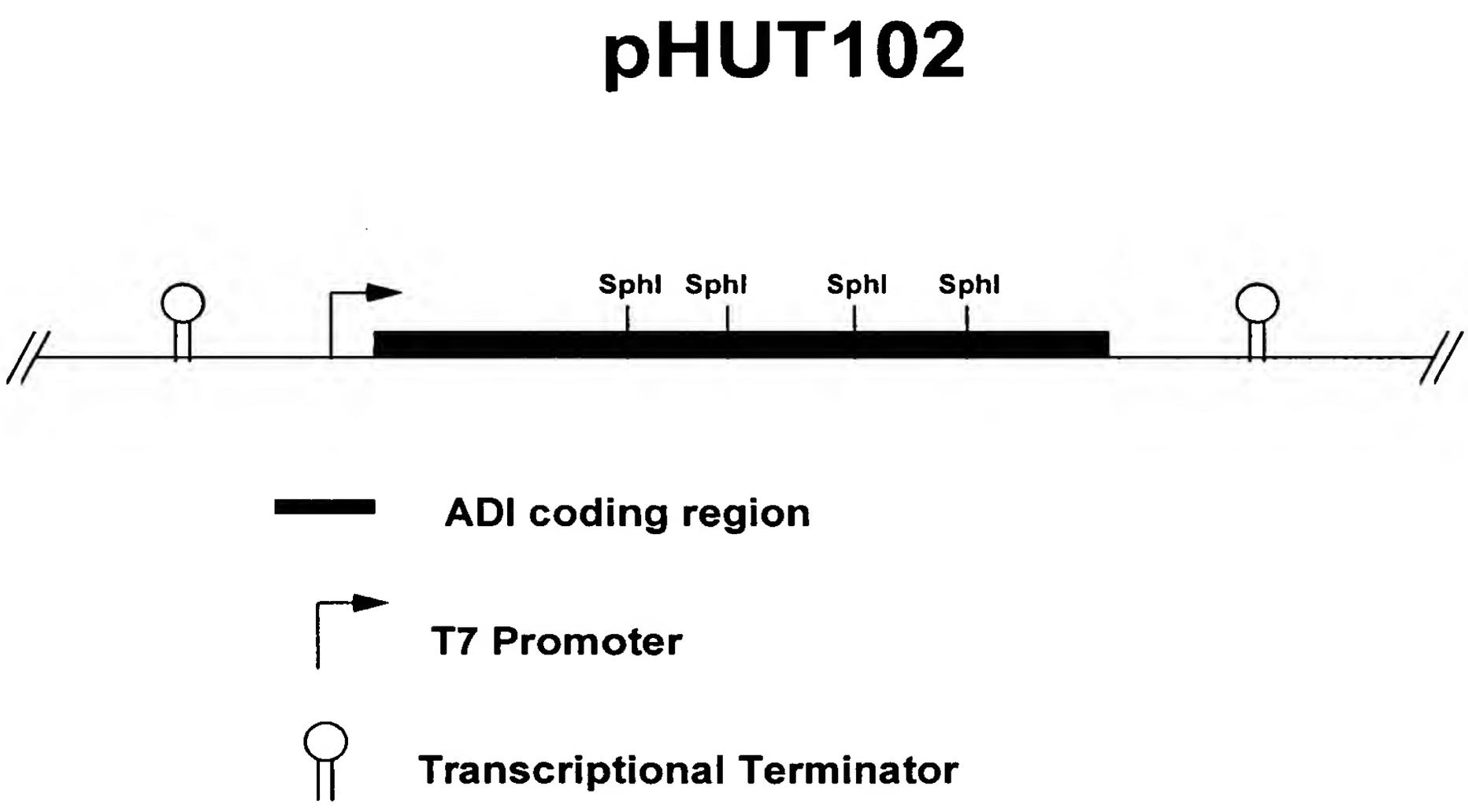

Figure 5: SDS-PAGE showing expression of HAL in *E. coli*.

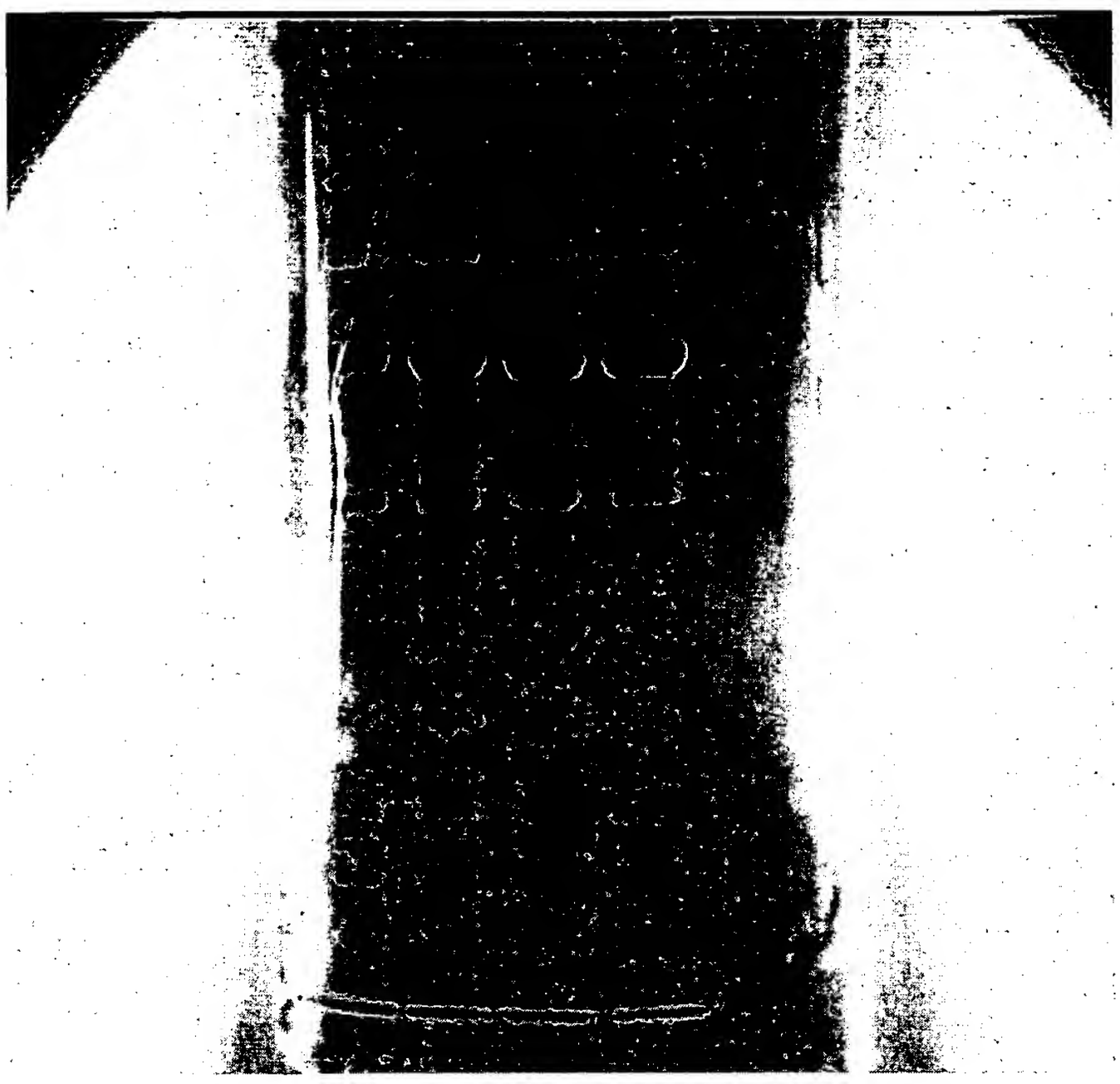

Figure 6: SDS-PAGE showing purification of HAL from *E. coli*

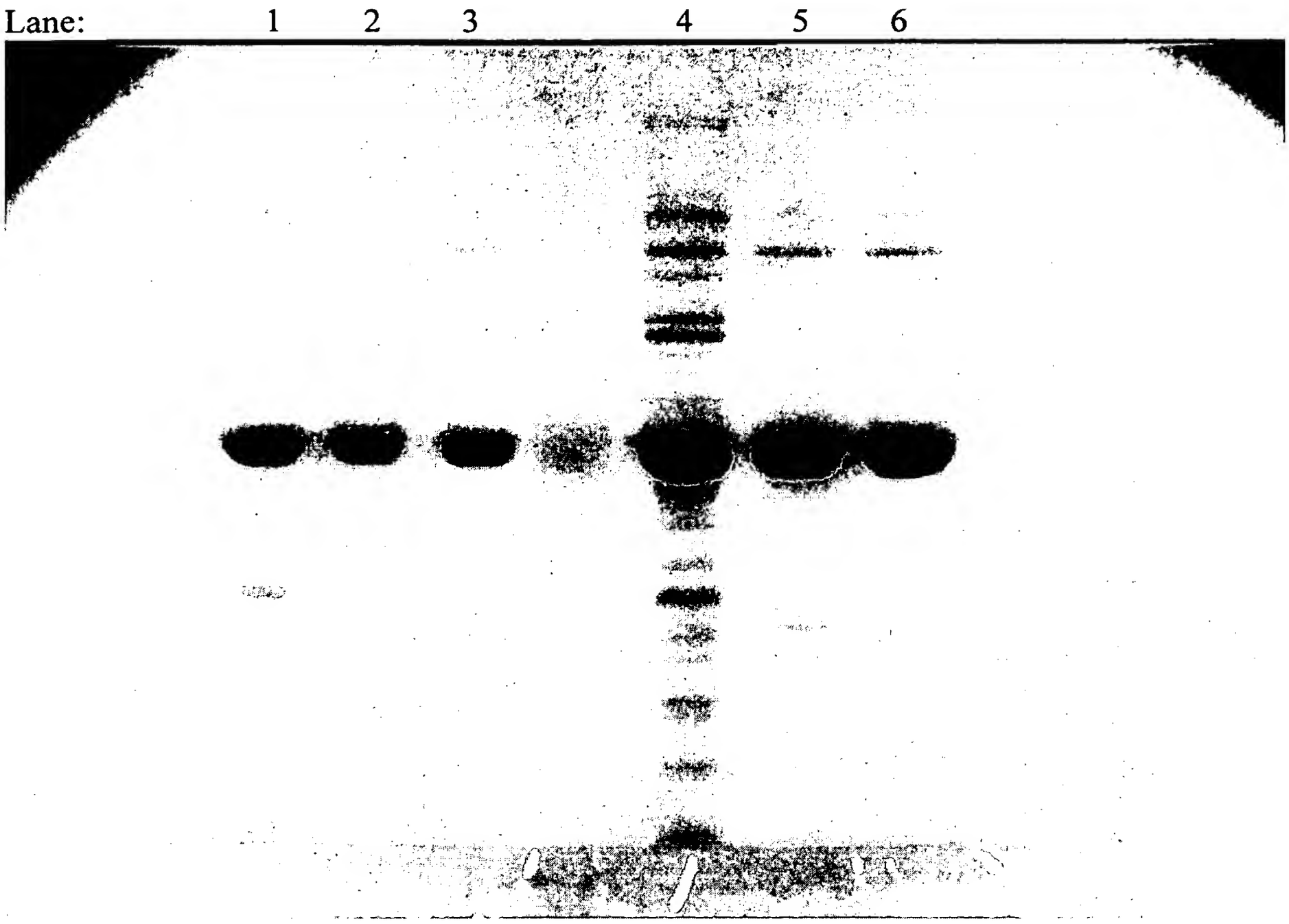

Figure 7: Effect of Temperature on HAL

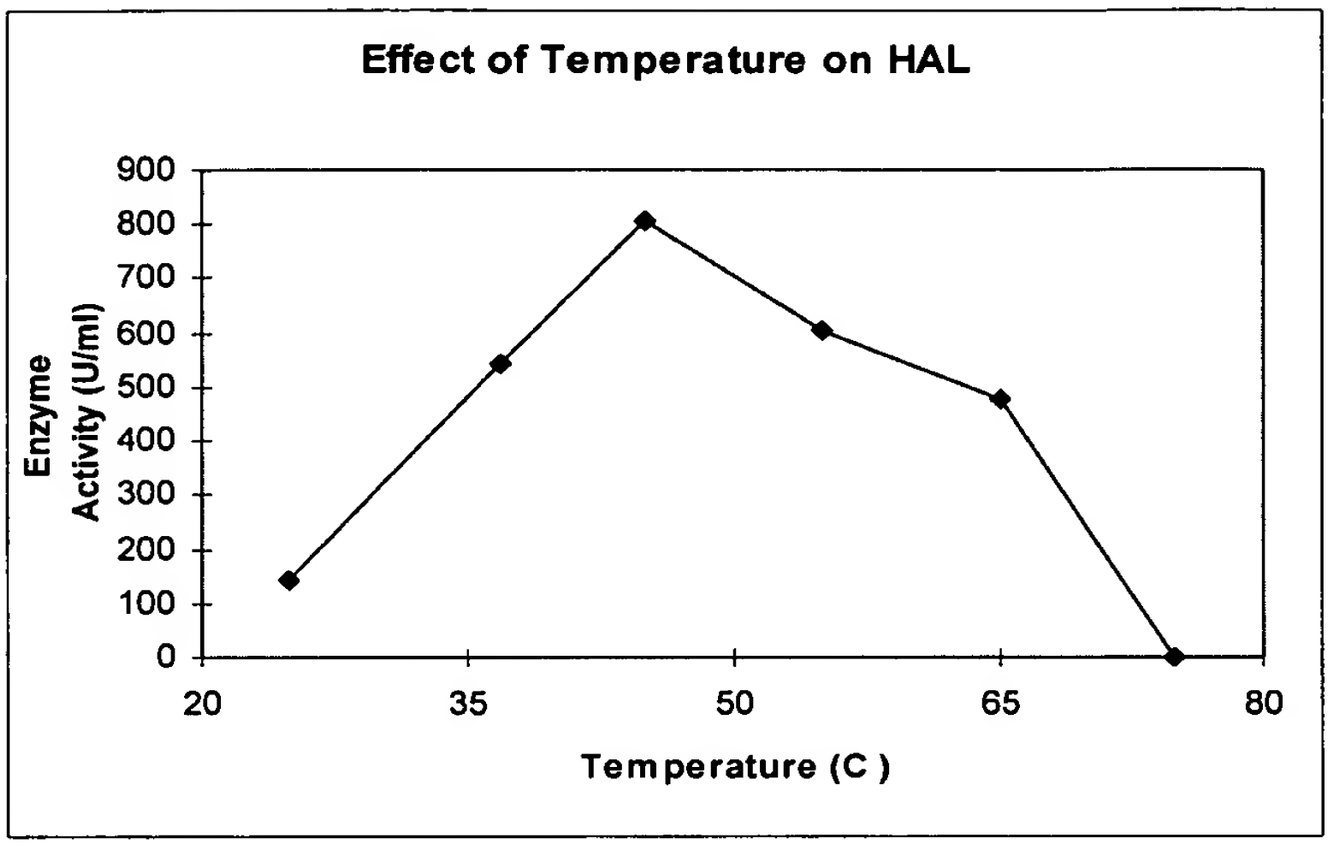

Figure 8: Effect of pH on HAL.

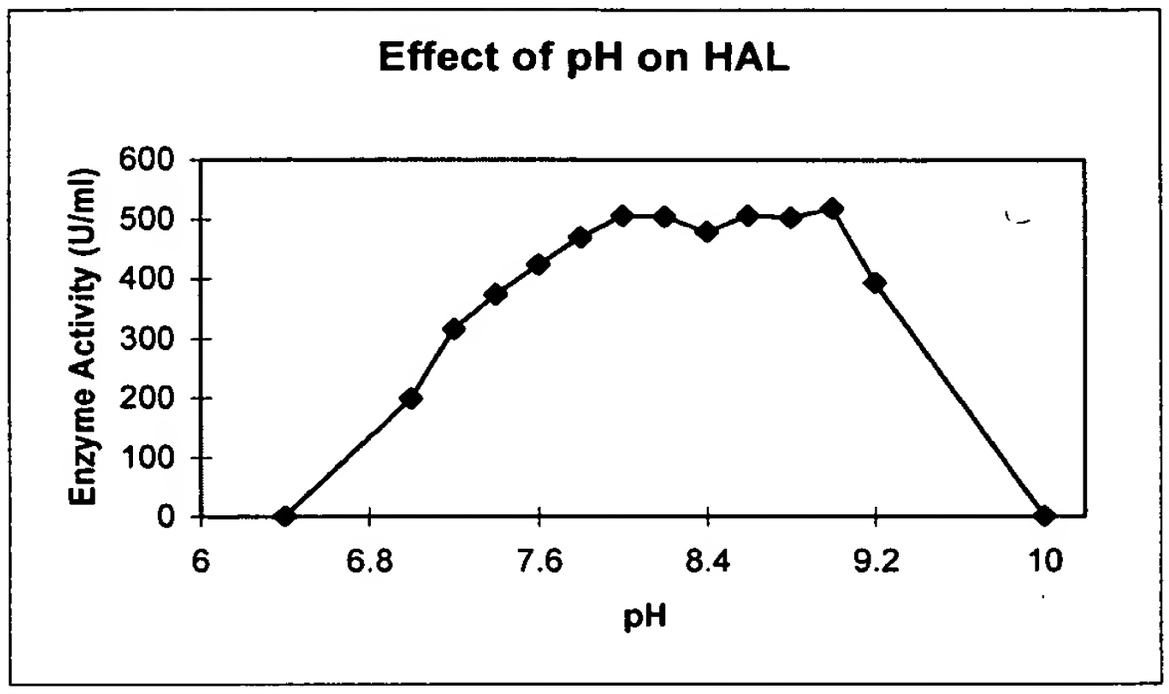

Figure 9: Effect of HAL and Histidinol on HSV.

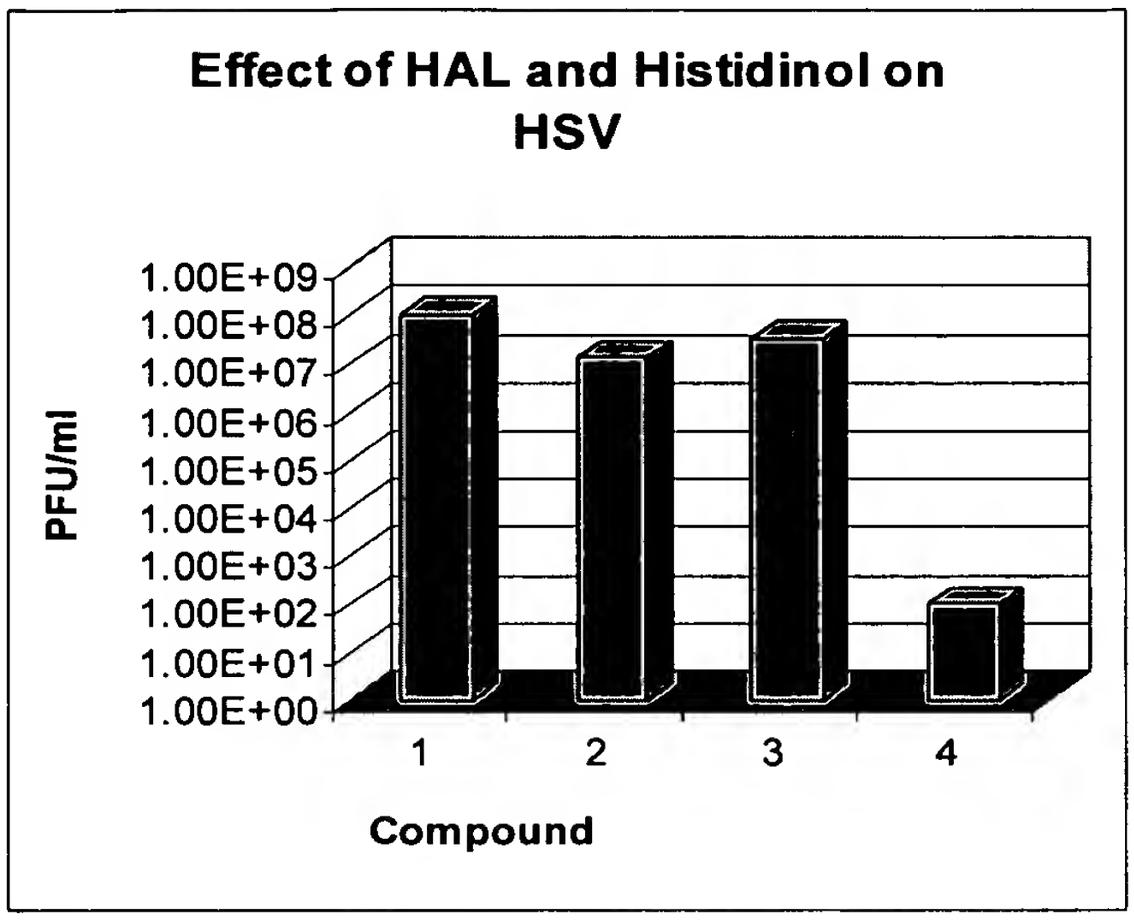

Figure 10: Effectiveness of L-histidinol as a Single Agent

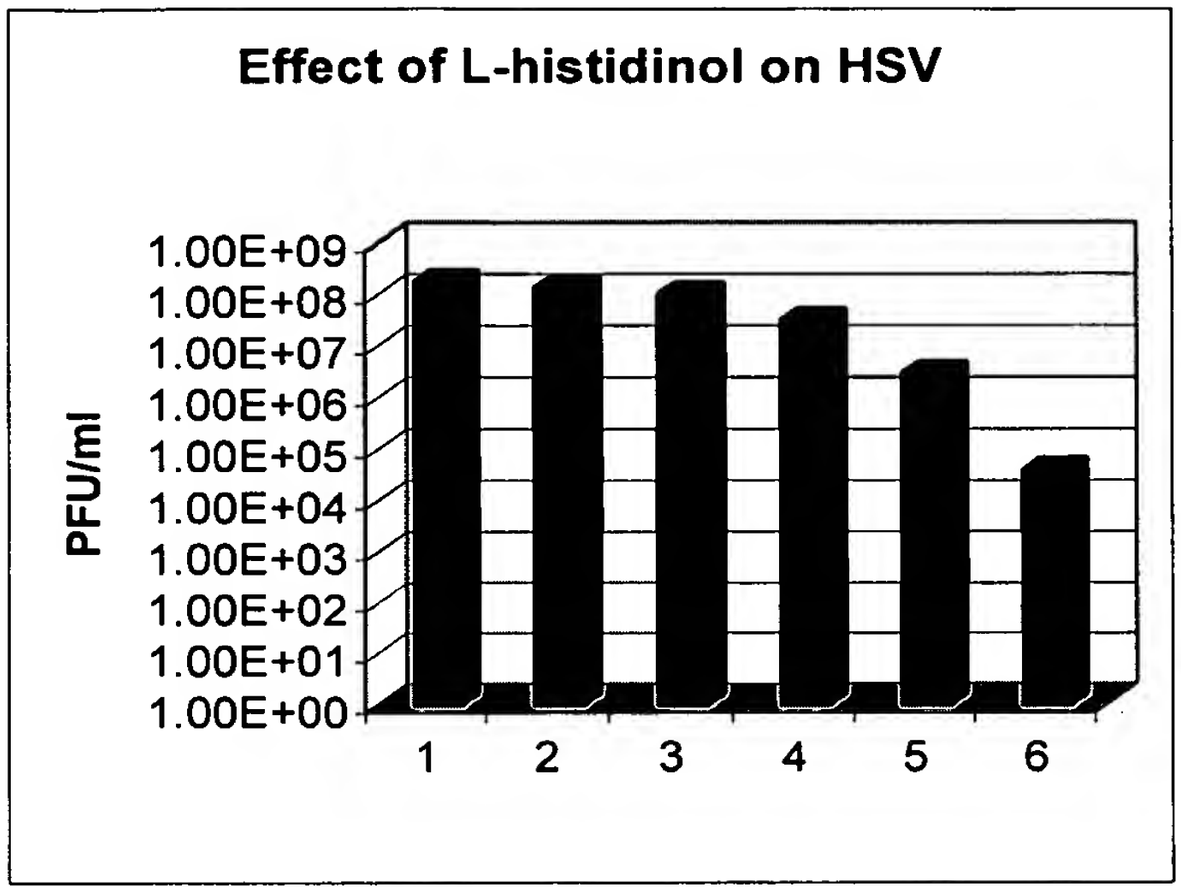

Figure 11: Effect of HAL and Histidinol on RSV.

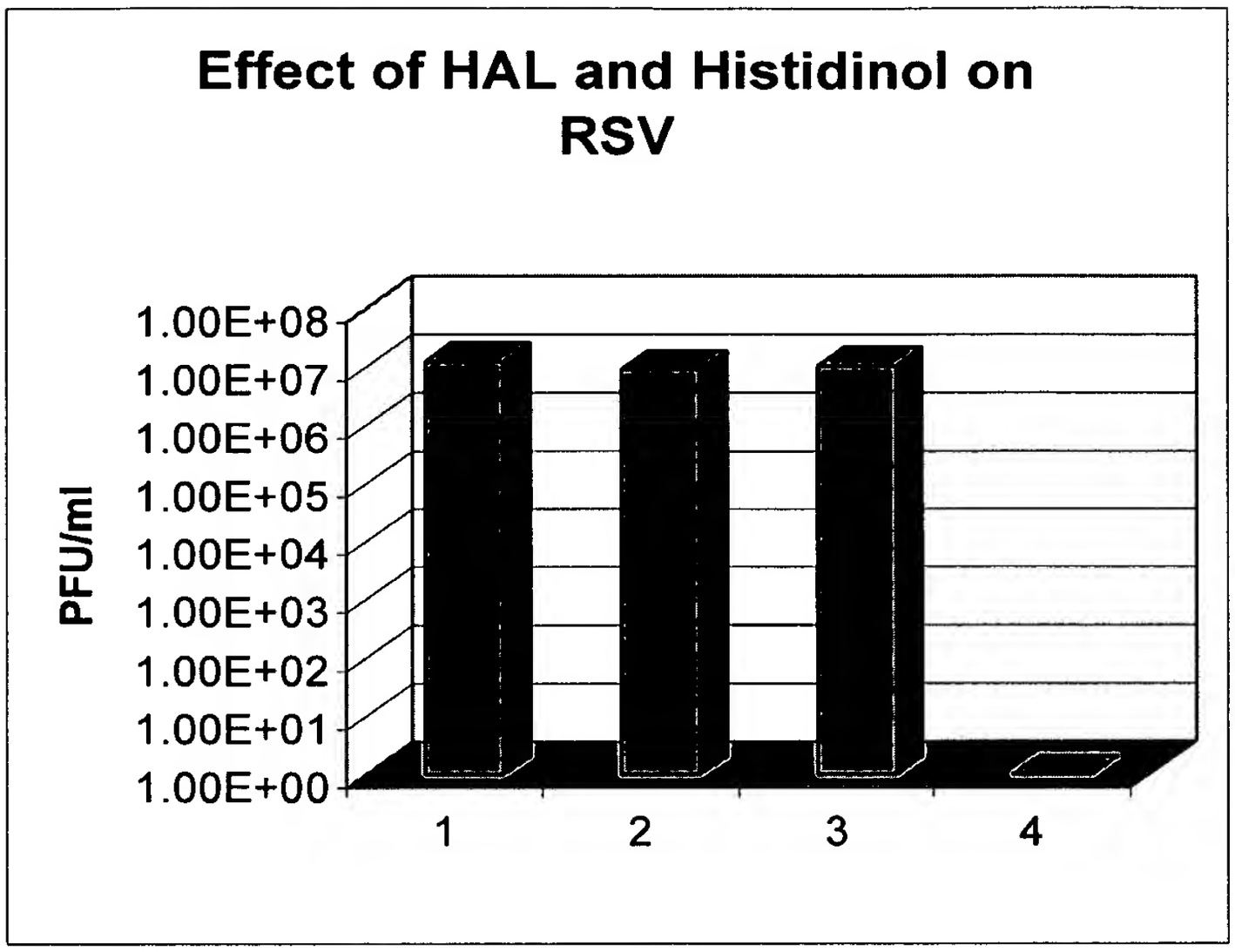

Figure 12: Effect of HAL on RMuLV.

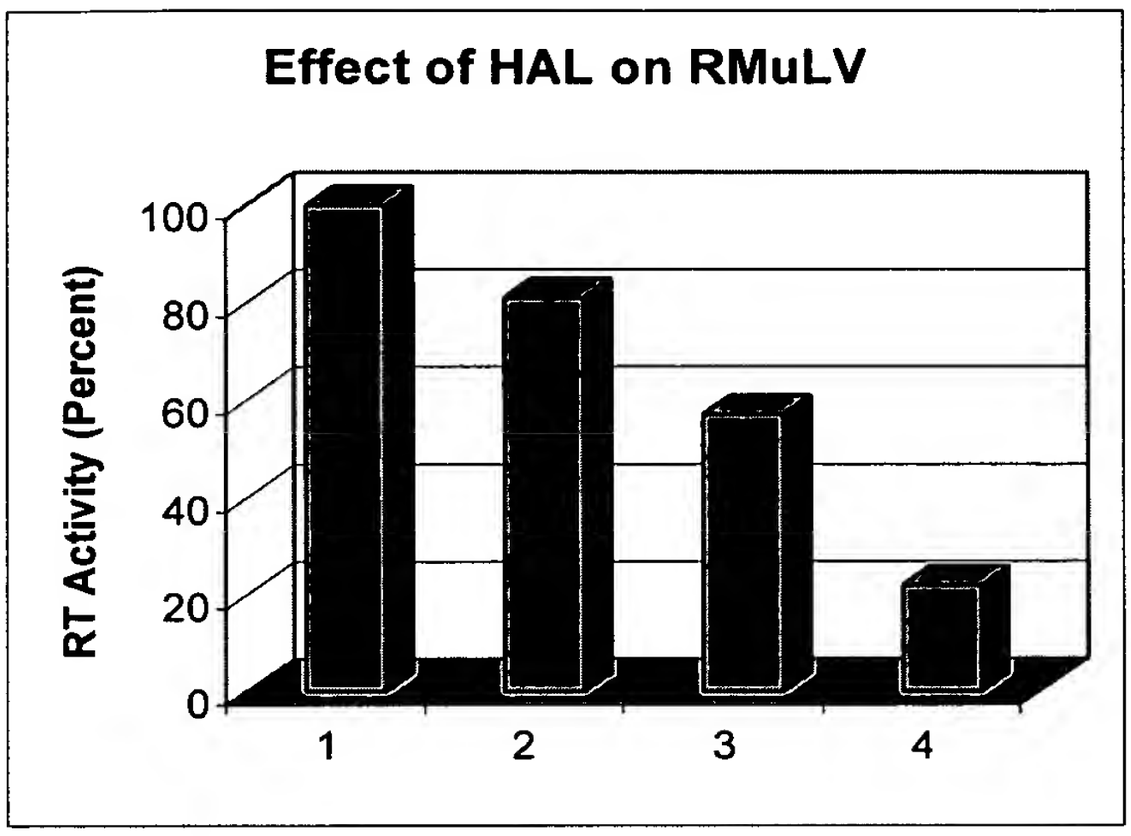

Figure 13A

```
HUTH_PSEPU      ------------------------------------------------------
-
HUTH_RHIME      ------------------------------------------------------
-
HUTH_MOUSE
MPRYTVHVRGEWLAVPCQDGKLTVGWLGREAVRRYMKNKPDNGGFTSVDEVQFLVHRCKG
HUTH_RAT
MPRYTVHVRGEWLAVPCQDGKLSVGWLGREAVRRYMKNKPDNGGFTSVDEVRFLVRRCKG
HUTH_HUMAN
MPRYTVHVRGEWLAVPCQDAQLTVGWLGREAVRRYIKNKPDNGGFTSVDDAHFLVRRCKG
HUTH_CAEEL      -MRLQVQIGTECVVVPCKP-DDTIHAVAKKSVEKLRRLRPK----
LPLADDYFEVRRTVG
HUTH_BACS       ------------------------------------------------------
-
HUTH_STRGR      ------------------------------------------------------
-
HUTH_CORY       ------------------------------------------------------
-


HUTH_PSEPU      ------------------------------------------------------
-
HUTH_RHIME      ------------------------------------------------------
-
HUTH_MOUSE      LGLLDNEDELEVALEDNEFVEVVIEGDVMS--------PDFIPSQPEGVFLYSKYR---
-
HUTH_RAT        LGLLDNEDLLEVALEDNEFVEVVIEGDVMS--------PDFIPSQPEGVFLYSKYR---
-
HUTH_HUMAN      LGLLDNEDRLEVALENNEFVEVVIEGDAMS--------PDFIPSQPEGVYLYSKYR---
-
HUTH_CAEEL
NSLLDPEDLVSDVLKDSDFIIVAASVEETEDAKEAKKQEEIDNARAEIEKIDNRRRKVSF
HUTH_BACS       ------------------------------------------------------
-
HUTH_STRGR      ------------------------------------------------------
-
HUTH_CORY       ------------------------------------------------------
-


HUTH_PSEPU      ------------
TELTLKPGTLTLAQLRAIHAAPVRLQLDASAAPAIDASVACVEQIIA
HUTH_RHIME      ------------
MTVILRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVA
HUTH_MOUSE      ----------
EPEKYIALDGDSLSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIK
HUTH_RAT        ----------
EPEKYIALDGDSLSTEDLVNLGKGHYKIKLTSIAEKKVQQSREVIDSIIK
HUTH_HUMAN      ----------
EPEKYIELDGDRLTTEDLVNLGKGRYKIKLTPTAEKRVQKSREVIDSIIK
HUTH_CAEEL
ADSLAPMVLAPPTKLLILDGNSLLPEDLVRCEKGECAIQLSMESEDRIRKARTFLEKIAS
HUTH_BACS       --------------
MVTLDGSSLTTADVARVLFDFEEAAASEESMERVKKSRAAVERIVR
HUTH_STRGR      ----------
MDMHTVVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAA
HUTH_CORY       ---------
MASAPQITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALAS
```

Figure 13B

HUTH_PSEPU
EDRTAYGINTGFGLLASTRIASHDLENLQRSLVLSHAAGIGAPLDDDLVRLIMVLKINSL
HUTH_RHIME
GNAPVYGINTGFGKLASIKIDSSDVATLQRNLILSHCCGVGQPLTEDIVRLIMALKLISL
HUTH_MOUSE
ERTVVYGITTGFGKFARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL
HUTH_RAT
ERTVVYGITTGFGKFARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL
HUTH_HUMAN
EKTVVYGITTGFGKFARTVIPINKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL
HUTH_CAEEL
EHRAVYGVTTGFGTFSNVTIPPEKLKKLQLNLIRSHATGYGEPLAPNRARMLLALRINIL
HUTH_BACS
DEKTIYGINTGFGKFSDVLIQKEDSAALQLNLILSHACGVGDPFPECVSRAMLLLRANAL
HUTH_STRGR
KPEPVYGVSTGFGALASRHIGTELRAQLQRNIVRSHAAGMGPRVEREVVRALMFLRLKTV
HUTH_CORY
ADTPVYGISTGFGALATRHIAPEDRAKLQRSLIRSHAAGMGEPVEREVVRALMFLRAKTL

HUTH_PSEPU
SRGFSGIRRKVIDALIALVNAEVYPHIPLKGSVGASGDLAPLATMSLVLLGEGKARYKGQ
HUTH_RHIME
GRGASGVRLELVRLIEAMLDKGVIPLIPEKGSVGASGDLAPLAHMAAVMMGHGEAFFAGE
HUTH_MOUSE
AKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_RAT
AKGYSGISLETLKQVIEVFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_HUMAN
AKGYSGISLETLKQVIEMFNASCLPYVPEKGTVGASGDLAPLSHLALGLVGEGKMWSPKS
HUTH_CAEEL
AKGHSGISVENIKKMIAAFNAFCVSYVPQQGTVGCSGDLCPLAHLALGLLGEGKMWSPTT
HUTH_BACS
LKGFSGVRAELIEQLLAFLNKRVHPVIPQQGSLGASGDLAPLSHLALALIGQGEVFFEGE
HUTH_STRGR
ASGHTGVRPEVAQTMADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEGEAEGPDG
HUTH_CORY ASGRS-
VRPVVLETMVGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHG

HUTH_PSEPU -
WLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSV
HUTH_RHIME -
RMKGDAALKAAGLSPVTLAAKEGLALINGTQVSTALALAGLFRAHRAGQAALITGALST
HUTH_MOUSE
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALTL
HUTH_RAT
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTL
HUTH_HUMAN
GWADAKYVLEAHGLKPVILKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTL
HUTH_CAEEL
GWQPADVVLKKNNLEPLELGPKEGLALINGTQMVTALGAYTLERAHNIARQADVIAALSL
HUTH_BACS -
RMPAMTGLKKAGIQPVTLTSKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERIASLTI
HUTH_STRGR
TVRPAGELLAAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALSL
HUTH_CORY
DIRPVPELFAEAGLTPVELAEKEGLALVNGTDGMLGQLIMALADLDELLDIADATAAMSV

Figure 13C

```
HUTH_PSEPU      EAVLGSRSPFDARIHE-ARGQRGQIDTAACFRDLLGDSSEVSLSHKNCD----
KVQDPYS
HUTH_RHIME      DAAMGSSAPFHPDIQH-CAAIRARSTRAAALRQLLTG-SPIRQSHIEGDE---
RVQDPYC
HUTH_MOUSE      EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_RAT        EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_HUMAN      EVLKGTTKAFDTDIHA-LRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_CAEEL      DVLKGTTRAYDPDIHR-IRPHRGQNLSALRLRALLHS-
EANPSQIAESHRNCTKVQDAYT
HUTH_BACS       EGLQGIIDAFDEDIHL-ARGYQEQIDVAERIRFYLSD-SGLTTSQGE-----
LRVQDAYS
HUTH_STRGR      EALLGTDKVLAPELHA-IRPHPGQGVSADNMSRVLAG-SGLTGHHQDDAP---
RVQDAYS
HUTH_CORY       EAQLGTDQVFRAELHEPLRPHPGQGRSAQNMFAFLAD-SPIVASHREGDG---
RVQDAYS


HUTH_PSEPU
LRCQPQVMGACLTQLRQAAEVLGIEANAVSDNPLVFAAEGDVISGGNFHAEPVAMAADNL
HUTH_RHIME      IRCQPQVDGACLDLLRSVAATLTIEANAVTDNPLVLSDN-
SVVSGGNFHAEPVAFAADQI
HUTH_MOUSE
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_RAT
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_HUMAN
LRCCPQVHGVVNDTIAFVKNIITTELNSATDNPMVFANRGETVSGGNFHGEYPAKALDYL
HUTH_CAEEL
LRCVPQVHGVVHDTIEFVREIITTEMNSATDNPLVFADREEIISGGNFHGEYPAKALDFL
HUTH_BACS
LRCIPQVHGATWQTLGYVKEKLEIEMNAATDNPLIFNDGDKVISGGNFHGQPIAFAMDFL
HUTH_STRGR      VRCAPQVNGAGRDTLDHAALVAGRELASSVDNPVVLPDG-
RVESNGNFHGAPVAYVLDFL
HUTH_CORY       LRCSPQVTGAARDTIAHARLVATRELAAAIDNPVVLPSG-
EVTSNGNFHGAPVAYVLDFL


HUTH_PSEPU      ALAIAEIGSLSERRISLMMDKHMS-
QLPPFLVENGGVNSGFMIAQVTAAALASENKALSH
HUTH_RHIME
ALAVCEIGAISQRRIALLVDPALSLRLPAFLAKKPGLNSGLMIAEVTSAALMSENKQLSH
HUTH_MOUSE      AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_RAT        AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_HUMAN      AIGIHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSENKALCH
HUTH_CAEEL      AIAVAELAQMSERRLERLVNKELS-
GLPTFLTPDGGLNSGFMTVQLCAASLVSENKVLCH
HUTH_BACS       KIAISELANIAERRIERLVNPQLN-
DLPPFLSPHPGLQSGAMIMQYAAASLVSENKTLAH
HUTH_STRGR
AIVAADLGSICERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAV
HUTH_CORY
AIAVADLGSIAERRTDRMLDPARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAV
```

Figure 13D

```
HUTH_PSEPU      PHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVPAIEWLGACQGLDLRKG—LKTS
HUTH_RHIME      PASVDSTPTSANQEDHVSMACHGARRLLQMTENLFSIIGIEALAAVQGIEFRAP—LTTS
HUTH_MOUSE      PSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRP—LKTT
HUTH_RAT        PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP—LKTT
HUTH_HUMAN      PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP—LKTT
HUTH_CAEEL      PSSVDSIPTSCNQEDHVSMGGFAARKALTVVEHVEAVLAMELLAACQGIEFLKP—LIST
HUTH_BACS       PASVDSIPSSANQEDHVSMGTIAARHAYQVIANTRRVIAIEAICALQAVEYRGI—EHAA
HUTH_STRGR
PASADSIPSSAMQEDHVSMGWSAARKLRTAVDNLARIVAVELYAATRAIELRAAEGLTPA
HUTH_CORY       PA-VDSIPSSAMQEDHVSLGWHAARKLPTSVANLRRILAVEMLIAGRALDLRAP—LKPG

HUTH_PSEPU      AKLEKARQALRSEVA-HYDRDRFFAPDIEKAVELLAKG---S-LTGLLPAGVLPSL---
-
HUTH_RHIME      PELQKAAAAVRGVSS-SIEEDRYMADDLKAAGDLVASG---R-LAAAVSAGILPKLEN-
HUTH_MOUSE      TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR
HUTH_RAT        TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR
HUTH_HUMAN      TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLEQKVWEVAAPYIEKYRMEHIPESR
HUTH_CAEEL      APLHKIYQLVRSVAP-
PLNEDRYMKPEIDAVLEMIRENRIWEAVLPHLETLEAMEELDPD
HUTH_BACS       SYTKQLFQEMRKVVP-SIQQDRVFSYDIERLTDWLKK----ESLIPDHQNKELRGMNI—
HUTH_STRGR      PASEAVVAALRAAGAEGPGPDRFLAPDLAAADTFVREG---R-LVAAVEPVTGPLA---
-
HUTH_CORY       PATGAVLEVLRSKVA-GPGQDRFLSAELEAAYDLLANG---S-VHKALEAHLPE-----
-


HUTH_PSEPU      ----------------------------
HUTH_RHIME      ----------------------------
HUTH_MOUSE      PLSPTAFSLESLRKNSATIPESDDL----
HUTH_RAT        PLSPTAFSLESLRKNSATIPESDDL----
HUTH_HUMAN      PLSPTAFSLQFLHKKSTKIPESEDL----
HUTH_CAEEL      ALRQFTKTPTGIVQDRSMIPISDDEESIE
HUTH_BACS       ----------------------------
HUTH_STRGR      ----------------------------
HUTH_CORY       ----------------------------
```

Figure 14A

```
                          1     [    .    .    .    .    :    .    .    . 80
   983831               100.0%  MASAPQITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALASADTPVYGISTGFGALATRHIAPEDRAKLQ
 1 SWALL:CAC21618        66.1%  ---MHTVVVGTSGVTASDVLAVARAGARIELSEEAVAALAAARSVVDALAAKPDPVYGVSTGFGALATRHISPELRGRLQ
 2 SWALL:HUTH_STRGR      65.4%  -MDMHTVVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGALASRHIGTELRAQLQ
 3 SWALL:HUTH_DEIRA      46.8%  -------MILDRDLNLEQFISVVRHGEQVELSAAARERIARARTVIEQIVEGDTPIYGVNTGFGKFENVQIDRSQLAQLQ
 4 SWALL:BAB16159        42.0%  -------------VPLHHLADIYWNNGSAKLDPSFDAAVLKGAARIAEIAAGNAPVYGINTGFGKLASIKIDAADLATLQ
 5 SWALL:Q9KWE4          42.0%  -------------VPLHHLADIYWNNGSAKLDPSFDAAVLKGAARIAEIAAGNAPVYGINTGFGKLASIKIDAADLATLQ
 6 SWALL:HUTH_BACSU      40.4%  -----MVTLDGSSLTTADVARVLFDFEEAAASEESMERVKKSRAAVERIVRDEKTIYGINTGFGKFSDVLIQKEDSAALQ
 7 SWALL:Q9KSQ4          42.2%  ---MLHLMIKPGQLSLKQLRQVSRSPVVLSLDPEAIPAIAESAQVVEQVISEGRTVYGINTGFGLLLANTKIAPQDLETLQ
 8 SWALL:Q9HU85          41.7%  ----MSLHLKPGQLTLADLRQAYLAPVRLSLDPSADAPIAASVACVENIIAEGRTAYGINTGFGLLLASTRISPADLEKLQ
 9 SWALL:Q9KBE6          39.3%  --MTNLKLLDGRSLSLHDLHRIIYEGETVGASDESMEKVKQSRKAVEQIVADEKIIYGITTGFGKFSDIFIDPDDVENLQ
10 SWALL:HUTH_PSEPU      41.7%  ----TELTLKPGTLTLAQLRAIHAAPVRLQLDASAAPAIDASVACVEQIIAEDRTAYGINTGFGLLASTRIASHDLENLQ
11 SWALL:HUTH_RHIME      40.6%  --------LRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVAGNAPVYGINTGFGKLASIKIDSSDVATLQ
12 SWALL:Q9HU90           40.7%  MSDLPSVVFGDGPLRWQELVAVARHGARLELSAAAWARIDNARAIVCRIVANGERAYGISTGLGALCDVLLEGEQLAELS
13 SWALL:HUTH_HUMAN      39.2%  KYREPEKYIELDGLTTEDLVNLGKGRYKIKLTPTAEKRVQKSREVIDSIIKEKTVVYGITTGFGKFA-RTVIPINKLQLQ
14 SWALL:HUTH_CAEEL      38.8%  VLAPPTKLLILDGNSPEDLVRCEKGECAIQLSMESEDRIRKARTFLEKIASEHRAVYGVTTGFGTFSNVTIPPEKLKKLQ
15 SWALL:Q9HLI6          41.0%  -----MIEIDGRSLRVEDVYAVAVEYDRVSISDDTLKAVEEKHEAFLKLINSGKTVYGVNTGFGSLLNVHIERDQEIELQ
16 SWALL:HUTH_MOUSE      38.6%  KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGITTGFGKFA-RTVIPANKLQLQ
17 SWALL:BAB29407         38.6%  KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGITTGFGKFA-RTVIPANKLQLQ
18 SWALL:HUTH_RAT         38.2%  KYREPEKYIALDGDSTEDLVNLGKGHYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGITTGFGKFA-RTVIPANKLQLQ
19 SWALL:AAG53586         39.8%  ---MNALTLTPGTLTLAQLRQVWQQPLQLTLDESAHEAINDSVACVEAIVAEGRTAYGINTGFGLLAQTRIATHDLENLQ
20 SWALL:Q9KKE0           38.9%  ----MGEMISLDGPLTWREIASIAEGASLDLSGPARLRIAQARRIVDALVERGIRGYGINTGVGALCDVIISRENQQALS
21 SWALL:Q9HQD5           42.2%  ------------------------------------------------------------MSDTRIDAADREALQ
```

Figure 14B

```
                      81     [       .       1       .       .       .       .       :       . 160
   983831           100.0%      RSLIRSHAAGMGEPVEREVVRALMFLRAKTLASGRTGVRPVVLETMVGMLNAGITPVVREYGSLGCSGDLAPLSHCALVL
 1 SWALL:CAC21618    66.1%      RNIVRSHAAGMGPRVEREVVRALMFLRLKTVCSGRTGVRPEVAQTMADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTL
 2 SWALL:HUTH_STRGR  65.4%      RNIVRSHAAGMGPRVEREVVRALMFLRLKTVASGHTGVRPEVAQTMADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTL
 3 SWALL:HUTH_DEIRA  46.8%      HNLIVSHAIGMGEPLPAEVVRGMLLLRAQSLSLGHSGVRVEVVELLLALLNADALPVVPSQGSVGASGDLAPLAHLALGL
 4 SWALL:BAB16159    42.0%      RNLILSHCCGVGAPLPENVVRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVIPEKGSVGASGDLAPLAHMSATM
 5 SWALL:Q9KWE4      42.0%      RNLILSHCCGVGAPLPENVVRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVIPEKGSVGASGDLAPLAHMSATM
 6 SWALL:HUTH_BACSU  40.4%      LNLILSHACGVGDPFPECVSRAMLLLRANALLKGFSGVRAELIEQLLAFLNKRVHPVIPQQGSLGASGDLAPLSHLALAL
 7 SWALL:Q9KSQ4      42.2%      KSIVLSHAAGIGELMSDETVRLMMLLKINSLARGYSGIRLEVIQALIELVNNQIYPCVPKKGSVGASGDLAPLAHMSTVL
 8 SWALL:Q9HU85      41.7%      RSIVLSHAAGVGEALDDAMVRLVMLLKVNSLARGFSGIRRKVIDALIALINAEVYPHIPLKGSVGASGDLAPLAHMSLVL
 9 SWALL:Q9KBE6      39.3%      HNLIYSHACGVGSPFPETVSRTMLVLRANALLKGFSGVRPLVIERLLALVNANIHPVIPQQGSLGASGDLAPLSHLALVL
10 SWALL:HUTH_PSEPU  41.7%      RSLVLSHAAGIGAPLDDDLVRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEVYPHIPLKGSVGASGDLAPLAHMSLVL
11 SWALL:HUTH_RHIME  40.6%      RNLILSHCCGVGQPLTEDIVRLIMALKLISLGRGASGVRLELVRLIEAMLDKGVIPLIPEKGSVGASGDLAPLAHMAAVM
12 SWALL:Q9HU90      40.7%      RNTLLSHACGVGEPLRDEQTRAIICAAVANYSQGKSGLDRSLVEGLLALLNHGITPQVPAQGSVGY---LTHMAHVGIAL
13 SWALL:HUTH_HUMAN  39.2%      VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEMFNASCLPYVPEKGTVGASGDLAPLSHLALGL
14 SWALL:HUTH_CAEEL  38.8%      LNLIRSHATGYGEPLAPNRARMLLALRINILAKGHSGISVENIKKMIAAFNAFCVSYVPQQGTVGCSGDLCPLAHLALGL
15 SWALL:Q9HLI6      41.0%      KNLIRSHSSGVGDYLENRYVRAIMAVRLNSLAAGYSAVSADLLNMMVEMLNRDVIPAVPKYGSVGASGDLAPLAHIGLAM
16 SWALL:HUTH_MOUSE  38.6%      VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGL
17 SWALL:BAB29407    38.6%      VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGL
18 SWALL:HUTH_RAT    38.2%      VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEVFNASCLSYVPEKGTVGASGDLAPLSHLALGL
19 SWALL:AAG53586    39.8%      RSLVLSHAAGVGEPLDDDIVRLMMVLKINSLARGFSGIRLSVIQALIALVNAGVYSVDPAKGSVGASGDLAPLAHMSLTL
20 SWALL:Q9KKE0      38.9%      RNIILSHACGVGDPLGRVEARAVMAAQIANLTHGYSGVRVETAEMLLALLNADIIPLIPSRGSVGY------LTHAALVL
21 SWALL:Q9HQD5      42.2%      ANLVRSHAAGAGSELDTAAVRALLVTRLNALAKGYSGIRERVLDVLVGLLNEGVHPVVPSRGSLGASGDLAPLAHMSRVL
```

Figure 14C

```
                              161    [         .         .         .         2         .         .         .         . 240
   983831                  100.0%    MGEGEATDAHGDIRPVPELFAEAGLTPVELAEKEGLALVNGTDGMLGQLIMALADLDELLDIADATAAMSVEAQLGTDQV
 1 SWALL:CAC21618           66.1%    MGEGDAEGPDGTVRPAGELLAAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLDTLYKSADITAALTMEALLGTDRV
 2 SWALL:HUTH_STRGR         65.4%    MGEGEAEGPDGTVRPAGELLAAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALSLEALLGTDKV
 3 SWALL:HUTH_DEIRA         46.8%    IGLGDI-EYQGQVRPAADVLAELGLSPVQLQAKEGLALINGTQLMGSLLALALHDAQVLLGTANLAAAMTVEARYGSHRP
 4 SWALL:BAB16159           42.0%    MGEGEAF-YQGVQMPSKDALAKAGLSPVVLAAKEGLALINGTQTSTALALAGLFRAHRAAQSALVTGALSTDAAMGSSAP
 5 SWALL:Q9KWE4             42.0%    MGEGEAF-YQGVQMPSKDALAKAGLSPVVLAAKEGLALINGTQTSTALALAGLFRAHRAAQSALVTGALSTDAAMGSSAP
 6 SWALL:HUTH_BACSU         40.4%    IGQGEVF-FEGERMPAMTGLKKAGIQPVTLTSKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERIASLTIEGLQGIIDA
 7 SWALL:Q9KSQ4             42.2%    LGEGQAR-YNGKIISGLEAMKIAGLEPITLAPKEGLALLNGTQASTAFALEGLFVAEDLFASATVCGAMSVEAALGSRRP
 8 SWALL:Q9HU85             41.7%    IGESRARH-RGEWLPAAEALAVAGLEPLTLAAKEGLALLNGTQVSTAYALRGLFEAEDLFAAATVCGGLSVEAMLGSRAP
 9 SWALL:Q9KBE6             39.3%    LGEGEVF-YKGTKTKASFALKEEEIEPITLTAKEGLALINGTQAMTAMGVIAYLEAEKLAFQSEIIASLTMEGLRGIIDA
10 SWALL:HUTH_PSEPU         41.7%    LGEGKAR-YKGQWLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSVEAVLGSRSP
11 SWALL:HUTH_RHIME         40.6%    MGHGEAFFAGERMKGDAALKA-AGLSPVTLAAKEGLALINGTQVSTALALAGLFRAHRAGQAALITGALSTDAAMGSSAP
12 SWALL:Q9HU90             40.7%    LGIGEVS-YRGSVVPAAAALAAEGLATVRLGAKDGLCLVNGTPCMTGLACLALDDAQRLAQWADVIGAMSFEALRGQLAA
13 SWALL:HUTH_HUMAN         39.2%    VGEGKMWSPKSGWADAKYVLEAHGLKPVILKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTLEVLKGTTKA
14 SWALL:HUTH_CAEEL         38.8%    LGEGKMWSPTTGWQPADVVLKKNNLEPLELGPKEGLALINGTQMVTALGAYTLERAHNIARQADVIAALSLDVLKGTTRA
15 SWALL:Q9HLI6             41.0%    MGEGKAF-FEGRLMDSARALEKAGLKPYQFKEKEGVALINGTSFMSGILSIAVMDAHDILENAIRSALLSFEALGGTSKA
16 SWALL:HUTH_MOUSE         38.6%    IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALTLEVLKGTTKA
17 SWALL:BAB29407           38.6%    IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALTLEVLKGTTKA
18 SWALL:HUTH_RAT           38.2%    IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTLEVLKGTTKA
19 SWALL:AAG53586           39.8%    LGEGKAR-YRGEWLPAATALQKAGLAPVTLAAKEGLALLNGTQASTAFALRGLFEAEDLFASAVVCGALTTEAVLGSRRP
20 SWALL:Q9KKE0             38.9%    IGHGSAMQGTERLSGADAL-ARLGLAPLRLEAKEGLSLVNGTPCATGLAALALARTERLFAWADAAAAMTYE-NLGSQAN
21 SWALL:Q9HQD5             42.2%    IGEGQA-DVAGERMPAAEALAAADLEPVTLQAKEGLALINGTQLTTGVAALALVDAERVLRSADTAGALTTEVTMSTTAS
```

Figure 14D

```
                           241     [         :         .         .         .         .         3         .         . 320
   983831            100.0%        FRAELHEPLRPHPGQGRSAQNMFAFLADSPIVASHREGDGRVQDAYSLRCSPQVTGAARDTIAHARLVATRELAAAIDNP
 1 SWALL:CAC21618     66.1%        LAPELHA-IRPHPGQAASAANMAAVLKGSGLTGHHQDDAPRVQDAYSVRCAPQVAGAGRDTMAHAGLVAERELAAAVDNP
 2 SWALL:HUTH_STRGR   65.4%        LAPELHA-IRPHPGQGVSADNMSRVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAALVAGRELASSVDNP
 3 SWALL:HUTH_DEIRA   46.8%        FQPDV-VGLRPHPGALAVAAELREFLAGSEIAPSHLTGDGKVQDAYSLRAVPQVHGATWDALAQAERVLAVEFASVTDNP
 4 SWALL:BAB16159     42.0%        FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCIRCQPQVDGACLDLLASVARTLEIEANAVTDNP
 5 SWALL:Q9KWE4       42.0%        FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCIRCQPQVDGACLDLLASVARTLEIEANAVTDNP
 6 SWALL:HUTH_BACSU   40.4%        FDEDIHLA-RGYQEQIDVAERIRFYLSDSGLTTS--QGELRVQDAYSLRCIPQVHGATWQTLGYVKEKLEIEMNAATDNP
 7 SWALL:Q9KSQ4       42.2%        FDPRIHR-VRGHRTQMDAATAYRHLLVSSEIGQSHSNCE-KVQDPYSLRCQPQVMGACLQQIRSAAEVLEVEANSVSDNP
 8 SWALL:Q9HU85       41.7%        FDARIHAA-RGQRGQIDVAAAYRDLLASSEVARSHEKCD-KVQDPYSLRCQPQVMGACLTQMRQAAEVLEIEANAVSDNP
 9 SWALL:Q9KBE6       39.3%        FDEQIHFA-RGYVEQVDVARRMESYLQDSQLTT--RQGELRVQDAYSLRCIPQVHGATWQTLRYVKEKLEIEMNAATDNP
10 SWALL:HUTH_PSEPU   41.7%        FDARIHEA-RGQRGQIDTAACFRDLLGDSSEVSSHKNCD-KVQDPYSLRCQPQVMGACLTQLRQAAEVLGIEANAVSDNP
11 SWALL:HUTH_RHIME   40.6%        FHPDIQHCAAIRARSTRAAA-LRQLLTGSPIRQSHIEGDERVQDPYCIRCQPQVDGACLDLLRSVAATLTIEANAVTDNP
12 SWALL:Q9HU90       40.7%        FDAEI-VALKPHPGMQRVAANLRALLAGSQVLENAR--GIRTQDALSIRSIPQIHGACRDQLAHARQIET-ELNSATDNP
13 SWALL:HUTH_HUMAN   39.2%        FDTDIHA-LRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKNIITTELNSATDNP
14 SWALL:HUTH_CAEEL   38.8%        YDPDIHR-IRPHRGQNLSALRLRALLNPSQIAESHRNCT-KVQDAYTLRCVPQVHGVVHDTIEFVREIITTEMNSATDNP
15 SWALL:Q9HLI6       41.0%        FTPWILGA-RPHLGQVAIGNRFREYLTGSDIV--KRADSVKVQDAYTLRCIPQVYGSVADVIDYVENVLSVEINSATDNP
16 SWALL:HUTH_MOUSE   38.6%        FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKDIITTELNSATDNP
17 SWALL:BAB29407     38.6%        FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKDIITTELNSATDNP
18 SWALL:HUTH_RAT     38.2%        FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKDIITTELNSATDNP
19 SWALL:AAG53586     39.8%        FDARIHE-VRGQRGQIDAAALFRHVLTDTSAIASHHNCD-KVQDPYSLRCQPQVMGACLTQMRQVAEVLLVESNAVSDNP
20 SWALL:Q9KKE0       38.9%        AFAELPLALRQSPGLSAVGEGLRDWLADSPMLAG--TAGTRTQDPLSLRAVPQVHGAARDAFGQVAEIVDRELASVTDNP
21 SWALL:Q9HQD5       42.2%        CAPAIHE-VRPHDGQAVSARHIRNLTAGSEVLDHHRDCD-RVQDAYSIRCLPQVHGAVRDALDHLRAAVATELNSATDNP
```

Figure 14E

```
                          321    [         .         .         :         .         .         .         .         . 400
   983831              100.0%      VVLPSGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIAERRTDRMLDPARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAE
 1 SWALL:CAC21618       66.1%      VVLPDGRVESNGNFHGAPVAYVLDFLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVGE
 2 SWALL:HUTH_STRGR     65.4%      VVLPDGRVESNGNFHGAPVAYVLDFLAIVAADLGSICERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSE
 3 SWALL:HUTH_DEIRA     46.8%      LIFPTGEVVSGGNFHGQPLAVTIDALKVAVAELGSISERRTEQLLNPALS-GLPAFLTPNGGLNSGFMIAQYTSAALVSE
 4 SWALL:BAB16159       42.0%      LVLSDNSVVSGGNFHAEPVAFAADQTALAVCEIGAIAQRRIALLVDPALSYGLPAFLSKKPGLNSGLMIAEVTSAALMSE
 5 SWALL:Q9KWE4         42.0%      LVLSDNSVVSGGNFHAEPVAFAADQTALAVCEIGAIAQRRIALLVDPALSYGLPAFLSKKPGLNSGLMIAEVTSAALMSE
 6 SWALL:HUTH_BACSU     40.4%      LIFNDGDVISGGNFHGQPIAFAMDFLKIAISELANIAERRIERLVNPQLN-DLPPFLSPHPGLQSGAMIMQYAAASLVSE
 7 SWALL:Q9KSQ4         42.2%      LVFADGDIISGGNFHAEPVAMAADNLALAIAEIGSLSERRMALLIDSALSK-LPPFLVDNGGVNSGFMIAQVTAAALASE
 8 SWALL:Q9HU85         41.7%      LVFAAGDVISGGNFHAEPVAMAADNLALALAEIGSLSERRISLMMDMHMSQ-LPPFLVANGGVNSGFMIAQVTAAALASD
 9 SWALL:Q9KBE6         39.3%      LIFDNGQVISGGNFHGQQIALAMDFLGIAMAELANISERRIERLVNPQLN-DLPPFLSAAPGVQSGVMILQYCAASLVSE
10 SWALL:HUTH_PSEPU     41.7%      LVFAAGDVISGGNFHAEPVAMAADNLALAIAEIGSLSERRISLMMDKHMSQ-LPPFLVENGGVNSGFMIAQVTAAALASE
11 SWALL:HUTH_RHIME     40.6%      LVLSDNSVVSGGNFHAEPVAFAADQIALAVCEIGAISQRRIALLVDPALSLRLPAFLAKKPGLNSGLMIAEVTSAALMSE
12 SWALL:Q9HU90         40.7%      LLLGTPEVVSQANPHGESVAMAADLLAIAVAELGGVAERRLDRLVNPLVS-GLPAFLVGKPGVNSGMMITQYVAASLAGE
13 SWALL:HUTH_HUMAN     39.2%      MVFANGETVSGGNFHGEYPAKALDYLAIGIHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE
14 SWALL:HUTH_CAEEL     38.8%      LVFADREIISGGNFHGEYPAKALDFLAIAVAELAQMSERRLERLVNKELS-GLPTFLTPDGGLNSGFMTVQLCAASLVSE
15 SWALL:Q9HLI6         41.0%      L-FNGEEVVSGGNFHGEPVALAADFLAIALTDLGNMVERRIARLVDTNLS-GLPPFLTPDSGLNSGYMIPQYTAAALCNR
16 SWALL:HUTH_MOUSE     38.6%      MVFASGETISGGNFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE
17 SWALL:BAB29407       38.6%      MVFASGETISGGNFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE
18 SWALL:HUTH_RAT       38.2%      MVFASGETISGGNFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAALVSE
19 SWALL:AAG53586       39.8%      LVFAANEMVFRGNFHAEPVAMAADNLALAIAEIGALSERRIALMMDKHMSQ-LPPFLVRNGGVNSGFMIAQVTAAALASE
20 SWALL:Q9KKE0         38.9%      AVAGSPEVHSQAHAVGAALGLAMDSLAVAVAEVAAISERRIDRLVNPLVS-GLPAFLAGDSGVSSGFMIAQYTAAALVAE
21 SWALL:Q9HQD5         42.2%      LVFPSGTVVSGGNFHGEVLALRLGYAASALAELAAISERRTDRLLNPETQEPLEPFLAPDSGLHSGLMIPQYTAASLVND
```

Figure 14F

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                          401   [       .       .       .       .       :       .       .       . 480
   983831              100.0%      NKRLAVPASVDSIPSSAMQEDHVSLGWHAARKLRTSVANLRRILAVEMLIAGRALDLRAPLKPGPATGAVLEVLRSKVAG
 1 SWALL:CAC21618       66.1%      LKRLAVPASADSIPSSAMQEDHVSMGWSAARKLRTAVDNLARVIAVELYAATRAIQLREGLTPAPASQAVVEAVRAAVEG
 2 SWALL:HUTH_STRGR     65.4%      MKRLAVPASADSIPSSAMQEDHVSMGWSAARKLRTAVDNLARIVAVELYAATRAIELRAALTPAPASEAVVAALRAAGAG
 3 SWALL:HUTH_DEIRA     46.8%      NKVLSHPASVDSIPTSANQEDHVSMGAHAARQLRQIVANVQTVLSIELLCAAQGLDFQQ-LRAGRGVQAAYEYVRTFVPT
 4 SWALL:BAB16159       42.0%      NKQMSHPASVDSTPTSANQEDHVSMACHGARRLLAMTDNLFGILGIEALAAVQGVELRGPLKTSPELEKAAAVLRSAVPV
 5 SWALL:Q9KWE4         42.0%      NKQMSHPASVDSTPTSANQEDHVSMACHGARRLLAMTDNLFGILGIEALAAVQGVELRGPLKTSPELEKAAAVLRSAVPV
 6 SWALL:HUTH_BACSU     40.4%      NKTLAHPASVDSIPSSANQEDHVSMGTIAARHAYQVIANTRRVIAIEAICALQAVEYRGIEHAASYTKQLFQEMRKVVPS
 7 SWALL:Q9KSQ4         42.2%      NKTLAHPASVDSLPTSANQEDHVSMATFAARRLRDMGENTRGILAVEYLAAAQGLDFRAPLKSSPRIEEARQILREKVPF
 8 SWALL:Q9HU85         41.7%      NKALAHPASVDSLPTSANQEDHVSMAPNAGKRLWAMAENVRGILAVEWLGACQGLDFREGLKSSPKLEQARRLLRDKVPY
 9 SWALL:Q9KBE6         39.3%      NKTLAHPASVDSIPSSANQEDHVSMGTIGSRHAYQIIQNVRNVLAIELICAMQAVDIRGREKMASFTKKILEKGREHVPY
10 SWALL:HUTH_PSEPU     41.7%      NKALSHPHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVLAIEWLGACQGLDLRKGLKTSAKLEKARQALRSEVAH
11 SWALL:HUTH_RHIME     40.6%      NKQLSHPASVDSTPTSANQEDHVSMACHGARRLLQMTENLFSIIGIEALAAVQGIEFRAPLTTSPELQKAAAAVRGVSSS
12 SWALL:Q9HU90         40.7%      NRQLAQPAVVDNFVTSALQEDHLSLGTSAALKLGRALENLRRILAIEYLLAAQAFEFLAPQRFGQGTAAAWGILRERVPA
13 SWALL:HUTH_HUMAN     39.2%      NKALCHPSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRPLKTTTPLEKVYDLVRSVVRP
14 SWALL:HUTH_CAEEL     38.8%      NKVLCHPSSVDSIPTSCNQEDHVSMGGFAARKALTVVEHVEAVLAMELLAACQGIEFLKPLISTAPLHKIYQLVRS-VAP
15 SWALL:Q9HLI6         41.0%      NKVLAYPSSADTIPTSANQEDHVSMGATGSLKLLEIIDNVRYIIAIEYLLGSQALEFTDK-GMSPSTRKIYEKIREKVEK
16 SWALL:HUTH_MOUSE     38.6%      SKALCHPSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRPLKTTTPLEKVYDLVRSVVRP
17 SWALL:BAB29407        38.6%      SKALCHPSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRPLKTTTPLEKVYDLVRSVVRP
18 SWALL:HUTH_RAT       38.2%      SKALCHPSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRPLKTTTPLEKVYDLVRSVVRP
19 SWALL:AAG53586        39.8%      NKGLCHPTSVDK-PPSANQEDHVSMAPAAGRRLWEMAGNTRGVLAVEWLAACQGADLRDGLTSSPLLEQARQSCGEQVAH
20 SWALL:Q9KKE0         38.9%      NRRLAAPASLDGGITSALQEDMLTHATPAAWKALSIVDNLERILAIELLAAHRPMSCSRKRRARRNAPLPFTGTYARRSP
21 SWALL:Q9HQD5         42.2%      LRSLGQP-TLDNASVSGAQEDHVSMSAGAAYNFREAVEKAATVVGVELLCGAQGREFLDPLALGAGTAAAYDLVR-EVSE
```

Figure 14G

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                          481    [        .         5         .  ] 513
   983831              100.0%      PGQDRFLSAELEAAYDLLANGSVHKALEAHLPA
 1 SWALL:CAC21618       66.1%      PGPDRHLAPDLAAADAFVRAGHLVAAAESVTGP
 2 SWALL:HUTH_STRGR     65.4%      PGPDRFLAPDLAAADTFVREGRLVAAVEPVTGP
 3 SWALL:HUTH_DEIRA     46.8%      LTEDRYFRPDLLRLRGELVSGRVAQAADTQAPA
 4 SWALL:BAB16159       42.0%      LEDDRYMATDLKAAIEVVASGALVSAISSGLPV
 5 SWALL:Q9KWE4         42.0%      LEDDRYMATDLKAAIEVVASGALVSAISSGLPV
 6 SWALL:HUTH_BACSU     40.4%      IQQDRVFSYDIERLTDWLKKESLIPDHQNKELR
 7 SWALL:Q9KSQ4         42.2%      YDKDRYFAPDIEKANALL-QLAVHNRLMPDQLL
 8 SWALL:Q9HU85         41.7%      YQEDRFFAPDIEAASQLLASGCLNALLPARLLP
 9 SWALL:Q9KBE6         39.3%      IDQDRMFAKDIERAAKWLKDGSWDFTKMREKER
10 SWALL:HUTH_PSEPU     41.7%      YDRDRFFAPDIEKAVELLAKGSLTGLLPAGLPS
11 SWALL:HUTH_RHIME     40.6%      IEEDRYMADDLKAAGDLVASGRLAAAVSAGLPK
12 SWALL:Q9HU90         40.7%      YDTDRWLAPDIASAAAILGERKSLARLAASIGD
13 SWALL:HUTH_HUMAN     39.2%      WIKDRFMAPDIEAAHRLLLEQKVWEVAAPYIEK
14 SWALL:HUTH_CAEEL     38.8%      PNEDRYMKPEIDAVLEMIRENRIWEAVLPHLET
15 SWALL:Q9HLI6         41.0%      LDHDRPPSFDIETIRKMMDKKEFISALP-----
16 SWALL:HUTH_MOUSE     38.6%      WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
17 SWALL:BAB29407       38.6%      WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
18 SWALL:HUTH_RAT       38.2%      WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
19 SWALL:AAG53586       39.8%      YDDDRFFAPDIEAAISLLNKGSLVGLLPAFL--
20 SWALL:Q9KKE0         38.9%      PIATIVR--------------------------
21 SWALL:Q9HQD5         42.2%      PAGDRALADDMAAVGDLVRAGLVEDAVARALDA
```

Figure 14H

KEY:

983831 : HAL
1 CAC21618 : Streptomyces coelicolor
2 HUTH_STRGR : Streptomyces griseus
3 HUTH_DEIRA : Deinococcus radiodurans
4 BAB16159 : Agrobacterium rhizogenes
5 Q9KWE4 : Agrobacterium rhizogenes
6 HUTH_BACSU : Bacillus subtilis
7 Q9KSQ4 : Vibrio cholerae
8 Q9HU85 : Pseudomonas aeruginosa
9 Q9KBE6 : Bacillus halodurans
10 HUTH_PSEPU : Pseudomonas putida
11 HUTH_RHIME : Rhizobium meliloti
12 Q9HU90 : Pseudomonas aeruginosa
13 HUTH_HUMAN : Human
14 HUTH_CAEEL : Caenorhabditis elegans
15 Q9HLI6 : Thermoplasma acidophilum
16 HUTH_MOUSE : Mouse
17 BAB29407 : Mus musculus (Mouse)
18 HUTH_RAT : Rat
18 AAG53586 : uncultured bacterium pCosAS1
20 Q9KKE0 : Rhizobium meliloti
21 Q9HQD5 : Halobacterium sp

Figure 15A

```
STRG      6   VVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGAL
"HAL"     7   ITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALASADTPVYGISTGFGAL
                 * ** ** ** ***** **   *    * **  *   ****    **** *******

STRG,     66  ASRHIGTELRAQLQRNIVRSHAAGMGPRVEREVVRALMFLRLKTVASGHTGVRPEVAQTM
HAL       67  ATRHIAPEDRAKLQRSLIRSHAAGMGEPVEREVVRALMFLRAKTLASGRTGVRPVVLETM
              * ***  * ** ***   ******** ************ ** *** ***** *  **

STRG      126 ADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEGEAEGPDGTVRPAGELLAAHGIA
HAL       127 VGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHGDIRPVPELFAEAGLT
                 ********* ******************** *******    *  **  ** *  *

STRG      186 PVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALSLEALLGTDKVLAPELH
HAL       187 PVELAEKEGLALVNGTDGMLGQLIMALADLDELLDIADATAAMSVEAQLGTDQVFRAELH
              **** ******* ******** * ******  *   ** *** * ** **** *   ***

STRG      246 A-IRPHPGQGVSADNMSRVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAA
HAL       247 EPLRPHPGQGRSAQNMFAFLADSPIVASHREGDGRVQDAYSLRCSPQVTGAARDTIAHAR
                 ******* ** **   ** *     *     ******* ** *** ** ***  **

STRG      305 LVAGRELASSVDNPVVLPDGRVESNGNFHGAPVAYVLDFLAIVAADLGSICERRTDRLLD
HAL       307 LVATRELAAAIDNPVVLPSGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIAERRTDRMLD
              *** ****   ******* * * ******************  ****** ****** **
```

Figure 15B

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STRG     365  KNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAVPASADSIPSSAMQEDHVSMG
HAL      367  PARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAVPASVDSIPSSAMQEDHVSLG
                **  ** ***** ***** ******** ** * ******** ************** *

STRG     425  WSAARKLRTAVDNLARIVAVELYAATRAIELRAAEGLTPAPASEAVVAALRAAGAEGPGP
HAL      427  WHAARKLRTSVANLRRILAVEMLIAGRALDLRAP--LKPGPATGAVLEVLRSKVA-GPGQ
              * ******* * ** ** ***   * **  ***   * * **  **   **   * ***

STRG     485  DRFLAPDLAAADTFVREGRLVAAVE
HAL      484  DRFLSAELEAAYDLLANGSVHKALE
              ****   * **       *    * *
```